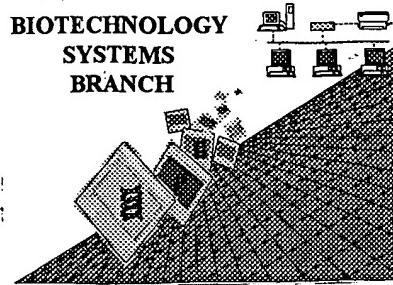


05-70  
12/17

## RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/821,782  
Source: O1PE  
Date Processed by STIC: 12/17/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.  
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:  
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE  
APPLICANT, WITH A NOTICE TO COMPLY or,  
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A  
NOTICE TO COMPLY  
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.  
PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)  
PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER  
VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND  
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by the treatment given to all mail coming via the Brentwood Mail Facility.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom, including:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>), EFS Submission User Manual - ePAVE)
2. U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:  
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7<sup>th</sup> Floor, Examiner Name,  
1911 South Clark Street, Crystal Mall One, Sequence Information, Arlington, VA 22202  
Or  
U.S. Patent and Trademark Office, 2011 South Clark Place, Customer Window, Box Sequence, Crystal Plaza Two,  
Lobby, Room 1B03, Arlington, Virginia 22202
4. Federal Express Delivery, 2011 South Clark Street, Crystal Plaza 2, Room 1B03-Mailroom, Box Sequence,  
Arlington, VA 22202

Raw Sequence Listing Error Summary

<u>ERROR DETECTED</u>	<u>SUGGESTED CORRECTION</u>	<u>SERIAL NUMBER:</u> <u>09/821,782</u>
<b>ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPIIA" HEADERS, WHICH WERE INSERTED BY PTO SOFT</b>		
1 <input type="checkbox"/> Wrapped Nucleic Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 <input type="checkbox"/> Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 <input type="checkbox"/> Misaligned Amino Numbering	The numbering under each 3 <sup>rd</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.	
4 <input type="checkbox"/> Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 <input type="checkbox"/> Variable Length	Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 <input type="checkbox"/> PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 <input type="checkbox"/> Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped	
8 <input type="checkbox"/> Skipped Sequences (NEW RULES)	Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
9 <input checked="" type="checkbox"/> Use of n's or Xaa's (NEW RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
10 <input type="checkbox"/> Invalid <213> Response	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
11 <input type="checkbox"/> Use of <220>	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence	
12 <input type="checkbox"/> PatentIn 2.0 "bug"	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
13 <input type="checkbox"/> Misuse of n	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	

n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

OIPE

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/821,782

DATE: 12/17/2001  
TIME: 15:11:29

Input Set : A:\821782seq.oct.txt  
Output Set: N:\CRF3\12172001\I821782.raw

*pg 1-7*  
Does Not Comply  
Corrected Diskette Needed

4 <110> APPLICANT: Kumar Verma, Sunil  
5 Singh, Lalji  
7 <120> TITLE OF INVENTION: UNIVERSAL PRIMERS FOR WILDLIFE IDENTIFICATION  
9 <130> FILE REFERENCE: U-013365-9  
11 <140> CURRENT APPLICATION NUMBER: 09/821782  
13 <141> CURRENT FILING DATE: 2001-03-29  
15 <160> NUMBER OF SEQ ID NOS: 255

## ERRORED SEQUENCES

17 <210> SEQ ID NO: 1  
19 <211> LENGTH: 25 *26 shown*  
21 <212> TYPE: DNA  
23 <213> ORGANISM: Artificial Sequence  
25 <220> FEATURE:  
27 <223> OTHER INFORMATION: Universal primer "mcb 398" for amplifying fragment of cytochrome b gene  
28 of animal species  
30 <400> SEQUENCE: 1  
E--> 32 taccatgagg acaaataatcta ttctg *(25) 26*  
411 <210> SEQ ID NO: 19  
413 <211> LENGTH: 328 *327*  
415 <212> TYPE: DNA  
417 <213> ORGANISM: gz21CL  
419 <220> FEATURE:  
421 <223> OTHER INFORMATION: DNA sequence generated from the known clouded leopard  
(Neofelis  
422 nebulosa) animal number 1 using primers mcb398 and mcb869  
424 <400> SEQUENCE: 19  
426 tgaatctgag gaggcttctc agtagacaaa gccaccctga cacgatttt cgcccccac  
427 ttcatcctcc catttatcat ctcagcctta gcagcagttc accttctatt tctccatgaa  
E--> 428 aaggatcca ataaccctc aggaatggta tccgatttag aaaaaatccc gttccacccg  
E--> 429 tactatacaa tcaaagatat cctaggctc ctatgttctaa ttcttagcgct cacactactt  
E--> 430 gttctattct ccccatgacct actaggagac cctgacaatt acactccgc caaccctcta  
E--> 431 aatacccttc cccatatcaa gcctgaat  
434 <210> SEQ ID NO: 20  
436 <211> LENGTH: 328 *327*  
438 <212> TYPE: DNA  
440 <213> ORGANISM: gz22CL  
442 <220> FEATURE:  
444 <223> OTHER INFORMATION: DNA sequence generated from the known clouded leopard  
(Neofelis  
445 nebulosa) animal number 2 using primers mcb398 and mcb869  
447 <400> SEQUENCE: 20  
449 tgaatctgag gaggcttctc agtagacaaa gccaccctga cacgatttt cgcccccac  
450 ttcatcctcc catttatcat ctcagcctta gcagcagttc accttctatt tctccatgaa  
E--> 451 aaggatcca ataaccctc aggaatggta tccgatttag aaaaaatccc gttccacccg

60  
120  
*180) 179*  
240  
300  
328  
nos. off  
due to  
above error

E--> 452 tactatacaa tcaaagatat cctaggcctc ctagttctaa ttcttagcgct cacactactt  
E--> 453 gttctattct ccccagacct actaggagac cctgacaatt acactccgc caaccctcta

(240)  
300 nos.  
off

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/821,782

DATE: 12/17/2001  
TIME: 15:11:29

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Output Set: N:\CRF3\12172001\I821782.raw

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959 <210> SEQ ID NO: 45  
961 <211> LENGTH: 472  
963 <212> TYPE: DNA  
965 <213> ORGANISM: Redunca fulvorufula  
967 <400> SEQUENCE: 45

969 tgccatgggg acaaataatcc ttctgaggag caacagttat cactaacctt ctctcagcaa  
970 tccccatacat cggcacaarc ctatgtaat gaatctgagg aggrttctca gtggataaaag  
971 caaccctcac tcgattcttc gccttccact ttatcctccc atttatcatc atagccctcg  
972 ctatagtcca cctactattc ctccatgaaa caggatccaa caaccccaaca ggggtttcat

E--> 973 cagayatgga caaaaatccca ttccacccat actacaccat caaagayatt cttagtgccc  
974 tactactaat cctggccctt acactattag tactattcac ccctgaccta ctggagacc  
975 cggacaatta caccccagca aacccactca acacacccccc tcacatcaaa ccagaatggg

E--> 976 acttcttatt ngcatacgca atcctacgat caatcccaa taaactagga gg item 9

328 off

numbering

off

→ see  
item 9

on

Error  
summary  
sheet

delete

hard page  
break  
472<210> 60

(hard page  
breaks are  
not  
permitted  
in  
computer  
readable  
form)

1238 <210> SEQ ID NO: 59  
1240 <211> LENGTH: 472  
1242 <212> TYPE: DNA  
1244 <213> ORGANISM: Balaenoptera bonaerensis  
1246 <400> SEQUENCE: 59

60

120

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420

472

item 9

W--> 1261 <213> ORGANISM: Balaenoptera borealis

E--> 1263 <210> SEQ ID NO:

E--> 1263 <400> SEQUENCE: 60

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1266 tccccatacat tggtaatcacc ctatgtaat ggatctgagg cggtttctct gttagataaaag  
1267 caacactaac acgtttttt gccttccact tcattctccc cttcattatt ctgcactatg  
1268 caatggtcca cctcattttc ctccatgaaa caggatccaa caaccccaaca ggtattccat  
1269 ccgacataga caaaaatccca ttccaccctt actacacagt taaagacatt ctggcgccc  
1270 tactactaat cctaacccta ctaataactaa ccctattcgc acccgacctg ctggagacc  
1271 cagacaacta caccccagca aatccactca gtaccccaac acacataaa ccagaatgat

60

120

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240

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420

472

item 9

E--> 1272 atttcctatt tgcatacgca atcctacgat caatcccaa caaattaggc gg

E--> 1275 <210> SEQ ID NO: 61

60

120

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472

item 9

item 9

item 9

item 9

item 9

item 9

E--> 1283 <400> SEQUENCE: 60 item 61 please edit

60

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180

240

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420

472

item 9

</div

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/821,782  
 DATE: 12/17/2001  
 TIME: 15:11:29

Input Set : A:\821782seq.oct.txt  
 Output Set: N:\CRF3\12172001\I821782.raw

1289 ccaacataga caaaatccca ttccacccct attacacaac taaagacatt ctaggcgccc 300  
 1290 tactactaat cctaacccta ctaatgctaa ccctattcgt acccgaccta cttggagacc 360  
 1291 cagacaacta cactccagca aatccactca gtaccccaac acacattaaa ccagaatgat 420  
 1292 atttcotatt tgcatacgca atcctacgtt caattcccaa caaatttaggc gg 472  
 2304 <210> SEQ ID NO: 13 113 ← change  
 2306 <211> LENGTH: 472  
 2308 <212> TYPE: DNA

E--> 2310 <213> ORGANISM: Hyperoodon ampullatus

2312 <400> SEQUENCE: 113  
 2314 taccctgagg acaaatatca ttctgaggcg caaccgtcat caccaatctc ctatccgcca 60  
 2315 ttccctatat cgccactacc ctatgttgaat gaatctgagg tggtttctcc gtagacaaag 120  
 2316 ccacattaac ccgccttttc gcctccact ttatcctccc attcattatt ctagccctag 180  
 2317 caatcgcca cctactattc ctccatgaaa caggatccaa caatcccaca ggaattccat 240  
 2318 ctgacataga caaaatcccg ttccacccat actacacaat caaagacact ctaggggccc 300  
 2319 tattactaat cctagtccca ctcacattaa ccctattcgc acccgaccta ctaggagacc 360  
 2320 ctgataacta taccggcga aaccctactca gcactccagc acacatcaaa ccagaatggt 420  
 2321 acttcttatt tgcatacgca atcctacgtt caattcccaa caaacttagga gg 472

E-->

2324 <210> SEQ ID NO: 114

3404 <210> SEQ ID NO: 169

3406 <211> LENGTH: 472

3408 <212> TYPE: DNA

3410 <213> ORGANISM: Afropavo congensis

3412 <400> SEQUENCE: 169

3414 tcccatgagg ccaaatatca ttctgagggg caactgtcat cacaaaccta tactcagcaa 60  
 3415 tcccttatat tggtaaaacc ctatgttgaat gggctgagg aggattctca gtgacaacc 120  
 3416 caaccctcac ccgattcttc gcctcacact ttcttctccc ctttctaatt ggggaatta 180  
 3417 caattatcca cctcacattc ttccatgaaa caggctaaaa caacccactg ggcacatctcat 240  
 3418 ccaattcaga taaaatccca ttccacccgt actactccct caaagatatac ctaggcttag 300  
 3419 cactcatgtt catccattc ctgacactag ccctactctc ccccaacctc ttaggtgatc 360  
 3420 cagaaaactt cacccagca aaccctctag taactccccca acacattaaa ccagaatggt 420

E--> 3421

atttcttatt tgcttatgcc atccttcgct caatcccaa caaacttagga gg

472 <210> 170

3423 <211> LENGTH: 472

3425 <212> TYPE: DNA

W-->

3427 <213> ORGANISM: Pavo muticus

E-->

3429 <210> SEQ ID NO:

3429 <400> SEQUENCE: 170

delete hard  
page break code

3431 tcccatgagg tcaaatagtca ttctgagggg caactgttat cacaaatctt ttctcagcaa 60  
 3432 tcccttatat tggacaaacc ctatgttgaat gagcctgagg gggattctca gtcgacaacc 120  
 3433 caaccctcac ccgattcttc gcctcacact ttcttctccc ctttctaatt gcagggattt 180  
 3434 caattatcca cctcacattc ttccatgaaa caggctaaaa taatccacta ggcacatctcat 240  
 3435 ccaactcaga caaaattccg ttccacccat actactccct caaagatatac ctaggcttaa 300  
 3436 ctcttatatt tatccattc ctaacactag ccctattctc ccccaatctc ttaggtgacc 360  
 3437 cagaaaactt tacccagca aaccctctag taaccccccgc acacattaaa ccagaatgat 420  
 E--> 3438 acttcttatt tgcttatgcc atccttcgctt caatcccaa caaacttagga gg 472

E-->

3441 <210> SEQ ID NO: 171

4283 <210> SEQ ID NO: 214

4285 <211> LENGTH: 23 22 (p.S)

4287 <212> TYPE: DNA

4289 <213> ORGANISM: Artificial Sequence

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/821,782

DATE: 12/17/2001  
TIME: 15:11:29

Input Set : A:\821782seq.oct.txt  
Output Set: N:\CRF3\12172001\I821782.raw

4291 <220> FEATURE:	
4293 <223> OTHER INFORMATION: Primer for amplifying a fragment of cytochrome b	
4294 gene of animal species in polymerase chain reaction	
4296 <400> SEQUENCE: 214	
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4301 <210> SEQ ID NO: 215	
4303 <211> LENGTH: 23	22
4305 <212> TYPE: DNA	
4307 <213> ORGANISM: Artificial Sequence	
4309 <220> FEATURE:	
4311 <223> OTHER INFORMATION: Primer for amplifying a fragment of cytochrome b	
4312 gene of animal species in polymerase chain reaction	
4314 <400> SEQUENCE: 215	
E--> 4316 atgcaaata ggaagtatca ttc	22
4319 <210> SEQ ID NO: 216	
4321 <211> LENGTH: 472	
4323 <212> TYPE: DNA	
4325 <213> ORGANISM: Aepyceros melampus	
4327 <400> SEQUENCE: 216	
4329 tgccatgagg acaaataatca ttctgaggag caacagtcat tacaaatctc ctctcagcaa	60
E--> 4330 tccccatatac tggtaaaaaac ctagtagaat gaatctgagg aggttttca gtagacaaaag	120
E--> 4331 caacccttac ccgatttttc gcyytccact tcatacytcc attcatcatt gggcactag	180
4332 ccatagttca cctactctt cttcacgaaa caggatctaa caaccctaca ggaatcttat	240
4333 cagattcaga taaaaattcca ttccaccctt actatactat traagacatc ctaggaatcc	300
4334 tattaataat tctagtccta atactcttag tactattcat acccgaccta cttaggagacc	360
E--> 4335 cagacaanma catcccgca aaccactca acaccctcc ccacatcaag cccgaatgg	420
E--> 4336 acttcctgtt ngcatacgca atcctacgat caatccccaa taaacttagga gg	472
4338 <210> SEQ ID NO: 217	
4340 <211> LENGTH: 472	
4342 <212> TYPE: DNA	
4344 <213> ORGANISM: Oreamnos americanus	
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4348 ttccgtgagg acaaataatca ttttgagggg ctacagtcat tactaatctc ctctcagcaa	60
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4350 caacccttac ccgatttttc gccttcaact tcatactttcc atttatcatc gaaaggccctag	180
4351 ccatagttaca cctactctt ctccacgaaa cagggtccaa taaccctaca ggaatctcat	240
4352 cagacacacaga caaaaatccc tttcatcattt attacacaat caaagatatac cttaggcggcc	300
4353 tattactaat tctagtttta ttactcttag tattattcac acctgaccta ctggagacc	360
4354 cagataacta caccctcgca aaccactca acactcccc tcacattaaa ccagaatgg	420
E--> 4355 atttnctatt ngcatacgca atcctacgat caatccccaa taaacttagga gg	472
4518 <210> SEQ ID NO: 226	
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4522 <212> TYPE: DNA	
4524 <213> ORGANISM: Bison bonasus	
4526 <400> SEQUENCE: 226	
p 6	
4528 taccatgagg acaaataatca ttttgaggag caacagtcat taccaacctc ctatcagcaa	60
4529 tccccatatac cggcacaaat ctagtcaat gaatctgagg cggattctca gtagacaaaag	120
4530 caacccttac ccgatttttc gccttcaact ttatcctccc atttattatc atagcaattt	180
4531 ccatagttca cctactattc ctccacgaaa caggttctaa caatccaaca ggaatttcct	240

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/821,782

DATE: 12/17/2001  
TIME: 15:11:29

Input Set : A:\821782seq.oct.txt  
Output Set: N:\CRF3\12172001\I821782.raw

4532	cagacacaga caaaaattcca ttccaccctt actataccat taaagacatc ctaggagcct	300
4533	tattactaat tctaactcta atactactag tactattcgc accggacctc ctcggagacc	360
4534	cagataacta caccccgca aatccactta acacacctcc ccacatcaa cccgaatgat	420
E--> 4535	<u>acttcttatt tgcataangca attttacggt caatccccaa caaacttagga gg</u> item 9	472
4794	<210> SEQ ID NO: 240	
4796	<211> LENGTH: 472	
4798	<212> TYPE: DNA	
4800	<213> ORGANISM: Rupicapra rupicapra	
4802	<400> SEQUENCE: 240	
4804	taccatgagg acagatatac ttctggggag caacagttat taccaacctc ctctcagcga	60
4805	tcccgtatat tggcacagac tttagtcaat gaatctgagg aggcttctcg gtagacaagg	120
4806	ctaccctcac ccgattcttt gccttccact tcatacctcc atttattcatt gcagccttag	180
4807	cccttagtcca cctactcttc ctccacgaaa caggatctaa caacccacaa ggaatccat	240
E--> 4808	<u>cagatgcgga caaaaatccca tttnaccctt attataccat caaagacatt ctgggcgcca</u> item 9	300
E--> 4809	<u>tactactaat cctcaccctc atactactag tactattnac acctgaccta ctcggagacc</u> item 9	360
4810	cagataatta caccccgacg aacccactca acacacccccc tcacattaaa cccgagtgat	420
4811	atttcttatt tgcataatgc attctacgat caatccccaa caaacttgga gg	472
4873	<210> SEQ ID NO: 244	
4875	<211> LENGTH: 472	
4877	<212> TYPE: DNA	
4879	<213> ORGANISM: Ovis vignei	
4881	<400> SEQUENCE: 244	
4883	taccatgagg acaaataatca ttctgaggag caacagttat taccaacctc ctttcagcaa	60
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4885	ctaccctcac ccgatttttc gccttccact ttatttccc attcatcatc gcagccctcg	180
4886	ctatagttca cctactcttc ctccacgaaa caggatccaa taacccacaa ggaattccat	240
E--> 4887	<u>cggacacacaga caaaaatcccc ttcnnnnnnn nnnnnnnnat taaagacatt ctgggtgcca</u> item 9	300
4888	tcctactaat cctcaccctc atgctgctag tactattcac gcctgactta cttggagacc	360
4889	cagacaacta caccccgacg aacccactca acactccccc tcacatcaa cctgaatgat	420
4890	atttcttatt tgcataatgc atcttacgat caatccctaa taaacttagga gg	472
5089	<210> SEQ ID NO: 255	
5091	<211> LENGTH: 472	
5093	<212> TYPE: DNA	
5095	<213> ORGANISM: Cervus elaphus canadensis	
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5100	ttccatatac tggcacaaac cttagtcaat gggctgagg aggcttca gtagataaaag	120
5101	caaccctaac ccgattcttc gccttccact ttattctcc atttacatc gcagcactcg	180
5102	ctatagtaca cttactcttc ctccacgaga caggatctaa taacccacaa ggaatccat	240
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5104	tacttctaat actcttcata atattactag tattattcgc accagatctg cttggagacc	360
5105	cagacaacta taccccgacg aatccactca acacacccccc tcacattaaa cctgaatgat	420
5106	atttcttatt tgcataatgc atcttacgat caatccctaa caaacttagga gg	472

see next page

09/021, 782

7

<210> 255

<211> 472

<212> DNA

<213> Cervus elaphus canadensis

<220>  
<223>

<400>(AB021096) → More up to <223> line

<400> always has the Sequence ID number as a response

<400> 255

VERIFICATION SUMMARY  
PATENT APPLICATION: US/09/821,782

DATE: 12/17/2001  
TIME: 15:11:31

Input Set : A:\821782seq.oct.txt  
Output Set: N:\CRF3\12172001\I821782.raw

L:32 M:254 E: No. of Bases conflict, LENGTH:Input:25 Counted:26 SEQ:1  
L:32 M:252 E: No. of Seq. differs, <211>LENGTH:Input:25 Found:26 SEQ:1  
L:428 M:254 E: No. of Bases conflict, LENGTH:Input:180 Counted:179 SEQ:19  
M:254 Repeated in SeqNo=19  
L:431 M:252 E: No. of Seq. differs, <211>LENGTH:Input:328 Found:327 SEQ:19  
L:451 M:254 E: No. of Bases conflict, LENGTH:Input:180 Counted:179 SEQ:20  
M:254 Repeated in SeqNo=20  
L:454 M:252 E: No. of Seq. differs, <211>LENGTH:Input:328 Found:327 SEQ:20  
L:973 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:45  
M:340 Repeated in SeqNo=45  
L:1255 M:254 E: No. of Bases conflict, LENGTH:Input:60 Counted:474 SEQ:59  
L:1255 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:8  
L:1255 M:252 E: No. of Seq. differs, <211>LENGTH:Input:472 Found:474 SEQ:59  
L:1263 M:282 W: Numeric Field Identifier Missing, <210> is required.  
L:1263 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:59 differs:60  
L:1275 M:214 E: (33) Seq.# missing, SEQ ID NO:60  
L:1283 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:61 differs:60  
L:2312 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:13 differs:113  
L:2324 M:216 E: (34) Seq.#s missing, SEQ ID NOS: 14 thru 113  
L:3421 M:254 E: No. of Bases conflict, LENGTH:Input:170 Counted:474 SEQ:169  
L:3421 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:8  
L:3421 M:252 E: No. of Seq. differs, <211>LENGTH:Input:472 Found:474 SEQ:169  
L:3429 M:282 W: Numeric Field Identifier Missing, <210> is required.  
L:3429 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:169 differs:170  
L:3441 M:214 E: (33) Seq.# missing, SEQ ID NO:170  
L:4298 M:252 E: No. of Seq. differs, <211>LENGTH:Input:23 Found:22 SEQ:214  
L:4316 M:252 E: No. of Seq. differs, <211>LENGTH:Input:23 Found:22 SEQ:215  
L:4330 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:216  
M:340 Repeated in SeqNo=216  
L:4355 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:217  
L:4535 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:226  
L:4808 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:240  
M:340 Repeated in SeqNo=240  
L:4887 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:244  
L:5097 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:255 differs:254